

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,471A

DATE: 18/14 4.75 TIME: 12:34:55

Input Set : A:\p02329.app

Output Set: N:\CRF4\03142003\J017471A.raw

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3 kilo> APPLICANT: Takano, Eriko
         Bibly Mervyn
6 <120 - TITLE OF INVENTION: Antibiotic Production
8 - 170 - FILE REFERENCE: 0380-F02329US1
10 - 140 - CUFRENT APPLICATION NUMBER: US 10/017,471A
11 - 141 - CUFFENT FILING DATE: 2001-10-23
13 - 150 - PRIER APPLICATION NUMBER: US 60/242,561
                                                                   The same prints prints to
   1919 PRIOR FILING DATE: 2000-10-23
16 - 160 - NUMBER OF SEQ ID NOS: 19
1- -1:0 - SCF:WAFE: PatentIn Ver. 2.1
23 - 113 - SEC ID NO: 1
21 - 211 - LENSTE: 18
12 - .12 - TYFE: IMA
13 - 113 - GRGANISM: Artificial Sequence
25 - 2.0 - FEATURE:
26 \times 13 \times \text{CTHER} INFOFMATION: Description of Artificial Sequence: Synthetic
          aligonuclectide
39 - 4 K - CEQUENCE: 1
                                                                             18
(ii) paddacated dsygdatg
32 - 210 - SED ID NO: 2
34 - . 11 - LENGTH: 24
RE - LAZ - TYPE: DNA
jo -. 12 - GR-ANISM: Artificial Sequence
38 - 1200 FEATURE:
19 - 122 - OFHER INFORMATION: Description of Artificial Sequence: Synthetic
          uligonupleotide
. : )
42 - 490 - BEQUENCE: 0
                                                                              24
43 proorgating cospisacso gsac
46 - III - SEQ ID NO: 3
47 - . 11 - LENGTH: 22
 43 ... TYPE: DNA
 43 - 115 - DREANISM: Artificial Sequence
51 + 12 - FEATURE:
5.2 \times 2.2 > 2 ITHER INFORMATION: Description of Artificial Sequence: Synthetic
           51.gonuclectide
 :73
 55 400> SEQUENCE: 3
                                                                              2.2
 36 postgoadit gigogacotg ac
 59 -310> SEQ ID NO: 4
 €0 211> LENGTH: 28
 61 - 2125 TYPE: DNA
 #2 -013> OF GANISM: Artificial Requence
 (4 °210→ FEATURE:
 85 /223/ 00 HEF INFORMATION: Description of Artificial Requence: Synthetic
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1ATE: 03 14 2 0 TIME: 11:34:55

FATENT APPLICATION: US/10/017,471A

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uligumusi erride 68 4 17 .E. ENZE: 4 ea da, ib sid fourdorrdd coard . . ng Kalib (ENSTE: 24 74 KATIDE TYPE: DNA 75 K213) - RUANISM: Artificial Sequence 37 W2. HY FEATURE: 78×2.30 THER INFORMATION: Description of Artificial Sequence: Synthetic **-** 9 l:gonuclectide 81 -4 0 ME. WENCE: 5 24 82 rations accept passed of the 85 rations accept to NC: 6 86 r211 rule NGTE: 24 81 - 212 TYPE: DNA 88 - 213 - -- F-MANISM: Artificial Sequence 90 - 2.9 - FEATURE: 91 - 2.3 - - THER INFORMATION: Description of Artificial Sequence: Synthetic Clyonablectide 9. 94 - 4.9 - BEQUENCE: 6 24 95 atogressit cotystiggs catg 98 0010 0 BEQ ID NO: 7 99 KT11 - LENGTH: 12 100 - Llu - TYPE: DNA 101 - J11 - CRGANISM: Artificial Sequence 104 - . 23 - CTHER INFORMATION: Description of Artificial Sequence: Synthetic .ligonus[ectide 105 100 - 40. - PERMENCE: 7 22 10% dagtagaggg otpoottggt ca 111 - 210 - REQ 10 NO: 8 119 - J1D - TYPE: DNA 114 - 113 - ORGANISM: Artificial Sequence 116 - 115 - FEATURE: 117 - 213 - THEE INFORMATION: Description of Artificial Sequence: Synthetic uligonuslectide 12. -400 CEQUENCE: 8 22 121 rasascist gottogggda tg 134 +310 + JEQ ID NO: 9 13: - 211 - : FNGTH: 22 120 - 21m - TYPE: DNA 12 - 21: - FGANISM: Artificial Sequence 123 - 2.1 - FEATURE: 130 2. · OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide 133 + 40.0 SEQUENCE: 9 22 134 typamooty ytoogytyya sa 137 -210> SEQ ID NO: 19

FATENT AFFILTATION: US/10/017,471A

1ATE: > 14:..... TIME: 11:34:88

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lat vall length: L4
ige - Mil - TYPE: DIA
147 -213 - ORGANISM: Artificial Sequence
145 KAZI - FEATURE:
143 K2Va+ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
          pligoruplestide
146 k400 % SEQUENCE: 10
                                                                         24
147 atrg Hoggt beigettige batg
150 k210k SEQ ID NO: 11
151 <211 / LEMGTH: 31
181 42120 IYEE: DNA
153 /213 / CRMANISM: Artificial Sequence
155 02.00 FEATURE:
156 + 2.3. CTHER INFORMATION: Description of Artificial Sequence: Synthetic
          ol.gomuslectide
157
159 - 4 ( - SE, UENCE: 11
                                                                         31
16 ) rater majo gigatogigg cagetiggia g
16 \pm \pm 210 \pm SEQ ID NO: 12
164 - 201 - LENGTH: 401
169 310 - TYPE: DNA
166 - 213 - OF-ANISM: Streptomyces coelicolor
16% + 40% + SEQUENCE: 12
16% payoungary goggtgacog agaacoggto acogcootto ggtatocago tgacogggaa 60
170 captur botgo aprotogotos gologacaag ogobatogga acoggoaatg ogottigito 120
171 satispaging grateggacy cagaattgat caaaactact gettegggea tgggteseec 130
172 hrandwatha totogatocog agetottoto tatogogogaa egitaagata dagaetogage 240
173 agrithurit statistics egggggagas atgaacaagg aggcaggcat ggccaagcag 3)0
174 maing mgcga thegraegeg geagacgate etggaegeeg eggegeaggt ettegagaag 360
175 regulatado addotigodas galcasggag atostoalagg t
 17a - 21a - SEQ ID NO: 13
 179 - 111 - LENGTH: 401
 180 - 110 - TYPE: DNA
 181 - 713 - OFGANISM: Streptomyces coelicclor
 183 4400 - SEQUENCE: 13
 184 acctigaçãa teleogigai egiggoagel tiggiagecel gelielegaa gaceligegee 60
 185 anggratora granogisty objectigog alogocoggi betgettigge eatgeotigee 120
 186 terriptica tyrotococo gggaaggata gaaaaaaaac ogotoagtot gtatottaac 180
 187 principguat adaquacage teggeateae atgatteetg ggggggaese atgeoegaag 240
 183 magnaghitt gateaattot gogtoogatg ocaabtogat ogaacaaabo goattgoogg 300
 143 thompatage gottgtecae eggaceaggg tgeaggaege gtteceggte agetggatae 360
 140 :: law.jgg.jgg tgareggtte teggteaceg cegteetgee e
 143 < 1 + SFQ ID NO: 14
  144 KA11 - LENGTH: 57
  195 kuli - TYPE: PRT
 196 <21% CAGANISM: Streptomytes coelicolor
  198 <400/ SEQUENCE: 14
 199 Met Pro Glu Ala Val Val Leu Ile Ash Ser Ala Ser Asp Ala Ash Ser
  202 lle Glu Gin Thr Ala Leu Pro Val Pro Met Ala Leu Val His Arg Thr
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PATENT APPLICATION: US/10/017,471A TIME: 11:34:16

LATE: : 14 L'is

input Set : A:\p02329.app

216 115 Arg The Ser Val Thr Ala Val Leu Fr. 212 K2105 SEQ ID NO: 18 213 <211> LENGTH: 37 214 K2125 TYPE: PRT 215 <213> CPGANISM: Streptomyces coelicolor 217 <400: SEQUENCE: 15 218 Met Ala Lys Gln Asp Arg Ala Ile Arg Thr Arg Gln Thr Ile Leu Asp 221 Ala Ala Ala Gln Val Phe Glu Lys Gln Gly Tyr Gln Ala Ala Thr Ile 7.22 20 :24 Thr Glu Ile Leu Lys 225 35 128 <210 - SEQ ID NO: 16 :29 -0011 - LENGTH: 215 134 -1212 - TYPE: PRT .31 0213 · ORGANISM: Streptomyces coelicolor 133 4400 - SEQUENCE: 16 133 Met Ala Lys Gln Asp Arg Ala Ile Arg Thr Arg Gln Thr Ile Leu Asp 10 1.35 1 137 Ala Ala Ala Gln Val Phe Glu Lys Gln Gly Tyr Gln Ala Ala Thr Ile 25 20 .40 Thr Glu Ile Leu Lys Val Ala Gly Val Thr Lys Gly Ala Leu Tyr Phe 45 40 ..41 35 147 His Phe Glm Ser Lys Glu Glu Leu Ala Leu Gly Val Phe Asp Ala Glm 60 55 . 44 50 14% Glu Pro Fro Gla Ala Val Pro Glu Gla Pro Leu Arg Leu Gla Glu Leu 75 70 . 47 65 ..49 Ile Asr Met Gly Met Leu Phe Cys His Arg Leu Arg Thr Asn Val Val 90 85 Ę. It! Ala Arg Ala Gly Val Arg Leu Ser Met Asp Gln Gln Ala His Gly Leu 110 105 100 150 Asp Arg Arg Gly Pro Phe Arg Arg Trp His Glu Thr Leu Leu Lys Leu 125 120 115 153 Leu Asr. Gln Ala Lys Glu Asn Gly Glu Leu Leu Pro His Val Val Thr 135 thel Thr Asp Ser Ala Asp Leu Tyr Val Gly Thr Phe Ala Gly Ile Gln Val 155 150 2+2 145 304 Val Ser Gln Thr Val Ser Asp Tyr Gln Asp Leu Glu His Arg Tyr Ala 170 247 Leu Leu Glr. Lys His Ile Leu Pro Ala Ile Ala Val Pro Ser Val Leu 185 180 268 270 Ala Ala Leu Asp Leu Ser Glu Glu Arg Gly Ala Arg Leu Ala Ala Glu 195 273 Let Ala Pro Thr Gly Lys Asp

TATE: or 14 class PATENT APPLICATION: US/10/017,471A TOME: 11:04:55

Input 200 : A:\p02329.app

. atput Fet: N:\CRF4\03142003\J017471A.raw

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īra kālis iemāle: 315
Ina Kalah TYFE: PAT
181 k218> ORGANISM: Streptomyces cuellotlor
282 k400% SEQUENCE: 10
283 Met Fro Glu Ala Val Val leu lle Ash Ser Ala Ser Asp Ala Ash Ser
188 Ile Glu Gln Thr Ala Leu Pro Val Pro Met Ala Leu Val His Ard Thr
200 Arg Val Gin Asp Ala Phe Pro Val Ser Trp Ile Pro Lys Gly Gly Asp
201 Arg Fhe Ser Val Thr Ala Val Leu Pro His Asp His Pro Phe Phe Ala
                            55
21:3 50
2.5 Pro Val His Gly Asp Arg His Asp Fro Lou Leu Ile Ala Glu Thr Leu
                        7.0
2:6 65
2*9 Arg Gln Ala Ala Met Leu Val Phe His Ala Gly Tyr Gly Val Pro Val
                                       30
                    8.5
3 I Gly Tyr His Phe Leu Met Thr Leu Asp Tyr Thr Cys His Leu Asp His
                                   105
         100
 3.4 Leu Gly Val Ser Gly Glu Val Ala Glu Leu Glu Val Glu Val Ala Cys
                                                   125
                               120
 311 Ser Gln Leu Lys Phe Arg Gly Gly Gln Pro Val Gln Gly Gln Val Asp
                           135
 369 130
 310 Trp Ala Val Arg Arg Ala Gly Arg Leu Ala Ala Thr Gly Thr Ala Thr
                                           155
            150
 311 145
 313 Thr Arg Fhe Thr Ser Fro Gln Val Tyr Arg Arg Met Arg Gly Asp Ph.e
                                        170
                    165
 316 Ala Thr Fro Thr Ala Ser Val Pro Gly Thr Ala Pro Val Pro Ala Ala
                                   185
                180
 313 Arg Ala Gly Arg Thr Arg Asp Glu Asp Val Val Leu Ser Ala Ser Ser
                                                    205
                                200
 5.10 195
 3... Gln Gln Asp Thr Trp Arg Leu Arg Val Asp Thr Ser His Pro Thr Leu
                                               220
                            215
 But Phe Gln Arg Pro Asn Asp His Val Pro Gly Met Leu Leu Leu Glu Ala
                        230
 1.8 Ala Arg Gln Ala Ala Cys Leu Val Thr Gly Pro Ala Pro Phe Val Pro
                                        250
                    245
 : Ser Ile Gly Gly Thr Arg Phe Val Arg Tyr Ala Glu Phe Asp Ser Pro
                                    265
                260
  1004 Cys Trp Ile 3lm Ala Thr Val Arg Pro Gly Pro Ala Ala Gly Leu Thr
                                280
  : 17 Thr Val Arg Val Thr Gly His Gln Asp Gly Ser Leu Val Phe Leu Thr
  295
  - +8 290
  :40 Thr Leu Ser Gly Pro Ala Phe Ser Gly
                         310
  944 <210> SEQ ID NO: 18
  448 K211> LENGTH: 262
  :46 <212> TYFE: FRT
  347 <213> ORGANISM: Streptomydes coelidolor
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VERIFICATION SUMMARY

FATENT APPLICATION: US/10/017,471A

Input Set : A:\p02329.app
 augus Set: N:\CRF4\03142003\J017471A.raw